

SEQUENCE LISTING

O I P E 14P/12
SEP 27 2006 <110>
PATENT & TRADEMARK OFFICE
<120> Cornell Research Foundation
Chang, Yung-Fu

<120> Ehrllichia canis genes and vaccines

<130> 1258-006 CIP

<140> 10/004,494

<141> 2001-11-02

<150> 09/358,322

<151> 1999-07-21

<160> 14

<170> PatentIn version 3.3

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<211> 5299

<212> DNA

<213> Ehrllichia canis

<220>

<221> gene

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<223> Protein translated from nucleotides 12 through 533 (cytochrome oxidase homolog).

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Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser Asn Ile		
35 40 45		
	tca aat tct aaa ata ggt aac act att att aaa gtc aga ttt aat gca	192
Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe Asn Ala		
50 55 60		
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Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His		
65 70 75 80		
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Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu		
85 90 95		
	aat cta ctt gat gag gac act tca gga atg gct gta tat aat gtt aca	336
Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr		
100 105 110		
	cca cat aaa gta gga aaa tat ttt aat aag gta gct tgt ttt tgt ttc	384
Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe		
115 120 125		
	acc aaa caa aca tta tac cct cat caa aaa act ata atg cca gta tca	432
Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser		
130 135 140		
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Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala Asp Val		
145 150 155 160		
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25

30

Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser Asn Ile
 35 40 45
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 50 55 60
 Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His
 65 70 75 80
 Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu
 85 90 95
 Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr
 100 105 110
 Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe
 115 120 125
 Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser
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 Lys Leu Ile Thr Leu Ser Tyr Val Phe Phe Lys Tyr Lys Glu
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 Asn His Ala Leu Ser Phe Asn Ile Lys Val Thr His Glu Lys Leu Asp
 20 25 30
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 Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro Ala Val
 35 40 45
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 Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly
 50 55 60
 tac tct gga tta gca cat ttt ttt gaa cac tta atg ttt agt gga aca 240
 Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr
 65 70 75 80

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ttc aat gca agc aca tct caa ttt tgt act ata tac tac gaa tta ata Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu Leu Ile 100 105 110	336
cca aaa caa tat tta tct ctt gca atg gat att gaa tca gac aga atg Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp Arg Met 115 120 125	384
cag aat ttt aag gtt acc gac aaa gca tta ata aga gaa caa aag gta Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln Lys Val 130 135 140	432
gtc tta gaa gaa aga aaa atg aga gtt gaa agc caa gca aaa aac ata Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys Asn Ile 145 150 155 160	480
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355	360	365	
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tat ttt tat ggc atg cat cta ata cta gga gta ccg cta tca gaa atc Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser Glu Ile 385 390 395 400			1200
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Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly 50 55 60			
Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr 65 70 75 80			
Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly Gly Asn 85 90 95			
Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu Leu Ile 100 105 110			
Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp Arg Met 115 120 125			
Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln Lys Val 130 135 140			
Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys Asn Ile 145 150 155 160			

Leu Glu Glu Glu Met Glu Asn Ala Phe Tyr Tyr Asn Gly Tyr Gly Arg
165 170 175

Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys Glu Val
180 185 190

Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala Ile Leu
195 200 205

Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu Ala Lys
210 215 220

Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser Ser Gln
225 230 235 240

Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr Leu Lys
245 250 255

Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln Ile Pro
260 265 270

Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu Ala Glu
275 280 285

Ile Leu Gly Ser Gly Lys Phe Ser Leu Leu Tyr Asn Asp Leu Val Ile
290 295 300

Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr Leu Thr
305 310 315 320

Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn Gly Ile
325 330 335

Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn Asn Tyr
340 345 350

Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys Tyr Lys
355 360 365

Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe Ile Ser
370 375 380

Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser Glu Ile
385 390 395 400

Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp Val Asn
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Leu Leu Pro Asn Gly Glu
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<210> 6
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Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr		
20 25 30		
aaa aat aaa ata cac tat cta tat gtt gaa cat cat aac cta cca aca	144	
Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr		
35 40 45		
att tcc tta aaa ttt gca ttc aag aaa gca gga tac gct tat gat gcc	192	
Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala		
50 55 60		
ttt gat aag caa gga ctt gca tac ttt aca tca aaa ata tta aac gaa	240	
Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu		
65 70 75 80		
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Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly		
85 90 95		
aaa ggt ata gac tta aaa ttt gat ata gac cta gac aat ttt tat ata	336	
Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile		
100 105 110		
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Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu		
115 120 125		
agt gat tgc ata ttc aac acc gtc aca gat caa gaa ata ttc aat aga	432	
Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe Asn Arg		
130 135 140		
ata ata gca gaa cag att gca cat gtt aaa tca tta tat tct gct cct	480	
Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro		
145 150 155 160		
gaa ttt ata gct aca aca gaa atg aat cac gct ata ttc aaa ggg cac	528	
Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His		
165 170 175		
cca tat tct aac aaa gtt tac ggg aca tta aat aca atc aat aat atc	576	
Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile		
180 185 190		
aac cag gaa gac gtt gca tta tat ata aaa aat agt ttt gac aag gaa	624	
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195 200 205		
caa atc gtt atc agc gca gca gga gat gta gat cca aca cag cta tca	672	
Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser		
210 215 220		

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aca gta cca tat cac agc aaa gac tat cat gca tca aac ttg ttc aat Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn 275 280 285	864
act atg cta ggc gga tta agt ctc aat tca ata tta atg ata gaa tta Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu 290 295 300	912
aga gac aag tta gga tta aca tac cat agt agc agt tca cta tct aac Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn 305 310 315 320	960
atg aat cat agt aat gtg cta ttt ggt aca ata ttc act gat aat acc Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr 325 330 335	1008
aca gta aca aaa tgt ata tcc gtc tta aca gat att ata gag cac att Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile 340 345 350	1056
aaa aag tat gga gtt gat gaa gac act ttt gca att gca aaa tct agt Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser 355 360 365	1104
att acc aac tct ttt att tta tct atg tta aat aac aat aat gtt agt Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn Val Ser 370 375 380	1152
gag ata ttg tta agc tta caa tta cac gat cta gat ccg agt tat att Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile 385 390 395 400	1200
aat aaa tac aat tct tac tac aaa gca ata aca ata gaa gaa gta aat Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn 405 410 415	1248
aaa att gcc aag aaa att tta tct aat gaa tta gta ata att gaa gta Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val 420 425 430	1296
gga aaa aac aat aac ata aat ggc aaa caa ata gat gct aaa aaa cac Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys Lys His 435 440 445	1344
ata ctt ggt Ile Leu Gly 450	1353

<210> 7
<211> 451
<212> PRT
<213> Ehrlichia canis

<400> 7

Met Arg Asn Ile Leu Cys Tyr Thr Leu Ile Leu Ile Phe Phe Ser Phe
1 5 10 15

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr
20 25 30

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr
35 40 45

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala
50 55 60

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu
65 70 75 80

Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly
85 90 95

Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile
100 105 110

Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu
115 120 125

Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe Asn Arg
130 135 140

Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro
145 150 155 160

Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His
165 170 175

Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile
180 185 190

Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp Lys Glu
195 200 205

Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser
210 215 220

Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly Asn Asn
225 230 235 240

Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr Leu Leu
245 250 255

Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala Thr Asp
260 265 270

Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn
275 280 285

Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu
290 295 300

Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn
305 310 315 320

Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr
325 330 335

Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile
340 345 350

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser
355 360 365

Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn Val Ser
370 375 380

Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile
385 390 395 400

Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn
405 410 415

Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val
420 425 430

Gly Lys Asn Asn Asn Ile Asn Gly Gln Ile Asp Ala Lys Lys His
435 440 445

Ile Leu Gly
450

<210> 8
<211> 663
<212> DNA
<213> *Ehrlichia canis*

<220>
<221> CDS
<222> (1)..(663)
<223> Protein translated from nucleotides 4,132 through 4,794 (mmpA).

<400> 8
atg aaa gct cat agc aca agt ata cgg aac ttt cag cct tta gaa aga 48
Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg
1 5 10 15

gct gct ata atc att gca gtg tta ggt tta gct gca ttc ttg ttt gct 96
Ala Ala Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala
20 25 30

gct gct gcc tgc agt gat cgt ttc caa aga ttg caa tta aca aat cca 144
Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro
35 40 45

ttt gta ata gca gga atg gtt ggc ctt gca gtt ctt tta gtt gct tcc 192
Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser

50	55	60	
tta aca gca gca tta agt ata tgc tta act aaa agt aag caa gtc aca Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr 65 70 75 80			240
caa cat gct att aga cat cgc ttt gga tac gag tca agc act tct tct Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser 85 90 95			288
tct gta ctg ctt gca ata tca ata att tct tta tta ctt gct gca gca Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala Ala 100 105 110			336
ttt tgt gga aag ata atg ggt aat gac aac cca gat cta ttc ttt agc Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser 115 120 125			384
aag atg caa gaa ctc tcc aat cca ctt gtt gtt gca gct att gta gcc Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala 130 135 140			432
gtt tct gtt ttc cta ctc tca ttc gta atg tat gct gca aag aac att Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile 145 150 155 160			480
ata agt cca gat aaa caa act cac gtt att ata tta tct aat caa caa Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln 165 170 175			528
act ata gaa gaa gca aaa gta gat caa gga atg aat att ttg tca gca Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala 180 185 190			576
gta ctc cca gca gct ggc att gac atc atg act ata gct tct tgt gac Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp 195 200 205			624
att tta gca gtg agc agc cgg gga tcc tct cag cat caa Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln 210 215 220			663

<210> 9
<211> 221
<212> PRT
<213> *Ehrlichia canis*

<400> 9

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg
1 5 10 15

Ala Ala Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala
20 25 30

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro
35 40 45

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser
50 55 60

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr
65 70 75 80

Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser
85 90 95

Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala Ala
100 105 110

Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser
115 120 125

Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala
130 135 140

Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile
145 150 155 160

Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln
165 170 175

Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala
180 185 190

Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp
195 200 205

Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln
210 215 220

<210> 10
<211> 417
<212> DNA
<213> Ehrlichia canis

<220>
<221> CDS
<222> (1)..(417)
<223> Protein translated from complementary sequence derived from
nucleotides 4,883 through 5,299 (partial lipoprotein signal
peptidase homolog).

<400> 10
gat cag gta agt aaa tgg tat gta gta aat ttg ata gga gat aaa ggt 48
Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp Lys Gly
1 5 10 15

gta ata gag ata tta agc ttc ttg cgc ttt act aca gtg tgg aat cct 96
Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp Asn Pro
20 25 30

gga att agt ttt ggt ata tta aat aac ttt gaa tat agt aat gtt gtt 144
Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn Val Val
35 40 45

ttt tgt agt atc tcg att ttg att act tgt gtt tta tgc tac tta ttt 192
Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr Leu Phe
50 55 60

ata gta cag cca cat tat aga tta cct ctt gta atc att att ggg ggg 240
Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile Gly Gly
65 70 75 80

tca ata gga aat atc ata gat aga ata aga tat ggt gct gtc tat gat Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val Tyr Asp 85 90 95	288
ttt ata gat ttt tat atc aat aac tta cat tgg cct gta ttc aac ctg Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe Asn Leu 100 105 110	336
gcg gat tct ttt ata ttt tta ggt ata gta ata ata atg gca aag agt Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala Lys Ser 115 120 125	384
aat aac cac atg aaa caa att aac tgt aac tcc Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser 130 135	417
 <210> 11 <211> 139 <212> PRT <213> <i>Ehrlichia canis</i>	
 <400> 11	
Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp Lys Gly 1 5 10 15	
Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp Asn Pro 20 25 30	
Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn Val Val 35 40 45	
Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr Leu Phe 50 55 60	
Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile Gly Gly 65 70 75 80	
Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val Tyr Asp 85 90 95	
Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe Asn Leu 100 105 110	
Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala Lys Ser 115 120 125	
Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser 130 135	
 <210> 12 <211> 41 <212> DNA <213> Artificial	
 <220> <223> oligonucleotide	
 <400> 12 aggcttgttcc agggtaaga agaatccaac gacaaaagct t	41

<210> 13
<211> 41
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 13 41
aagcttttgt cgttggattc ttcttcaccc tgaacttgcc a

<210> 14
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Nonapeptide sequence VQGEESNDK from IL-1beta

<400> 14

val Gln Gly Glu Glu Ser Asn Asp Lys
1 5